LISTING OF CLAIMS

1. (*currently amended*): A eukaryotic host cell transformed with a nucleic acid construct comprising a nucleotide sequence encoding a xylose isomerase comprising an amino acid sequence that has at least 70 % sequence identity with the amino acid sequence of SEQ ID NO: 1, wherein, when ~~whereby~~ the nucleic acid construct is expressed, ~~upon transformation of the host cell, confers to~~ the host cell acquires the ability to grow on xylose as a carbon source.

2. (*currently amended*): A transformed host cell according to claim 1, wherein the host cell is a yeast cell~~, preferably a yeast that belongs to one of the genera: *Saccharomyces*, *Kluyveromyces*, *Candida*, *Pichia*, *Schizosaccharomyces*, *Hansenula*, *Kloeckera*, *Schwanniomyces*, and *Yarrowia*~~.

3. (*currently amended*) The yeast ~~A transformed host~~ cell according to claim [[2]] 18 ~~, wherein the yeast belongs to one~~ that is a member of ~~the~~ a species selected from the group consisting of[[:]] *S. cerevisiae*, *S. bulderi*, *S. barnetti*, *S. exiguus*, *S. uvarum*, *S. diastaticus*, *K. lactis*, *K. marxianus*, and *K. fragilis*.

4. (*currently amended*): A transformed host cell according to claim 1, wherein the host cell is a filamentous fungus~~, preferably a filamentous fungus that belongs to one of the genera: *Aspergillus*, *Trichoderma*, *Humicola*, *Acremonium*, *Fusarium*, and *Penicillium*~~.

5. (*currently amended*) A transformed host cell of claim 1~~according to any one of the preceding claims, whereby~~ wherein the nucleotide sequence ~~encoding a xylose isomerase~~ is operably linked to a promoter that drives ~~causes sufficient~~ expression of the xylose isomerase in the host cell, such that ~~to confer to~~ the host cell ~~the ability to isomerise~~ can isomerize xylose [[in]]to xylulose.

6. (*currently amended*) A transformed host cell according to claim 5 [[6]], wherein ~~whereby~~ the promoter is insensitive to catabolite repression in the host cell.

7. (*currently amended*) A transformed host cell according to claim 1 ~~any one of the preceding claims, whereby the host cell~~ that further comprises a genetic modification that results in ~~a characteristic selected from the group consisting of~~:

(a) increased transport of xylose into the host cell;

(b) increased xylulose kinase activity;

(c) increased flux of the pentose phosphate pathway;

(d) decreased sensitivity to catabolite ~~respression~~ repression;

(e) increased tolerance to ethanol, osmolarity or organic acids; or ~~and,~~

(f) decreased ~~reduced~~ production of by-products,

which increase or decrease is in comparison to a similar cell that does not comprise said genetic modification.

8. (*currently amended*) A transformed host cell according to claim 7, wherein the genetic modification ~~consist of~~ results in (i) overexpression of an endogenous gene[[s]], (ii) expression of a heterologous gene[[s]], or (iii) a combination of (i) and (ii) ~~thereof~~, and

~~whereby~~ wherein the gene being expressed or overexpressed is selected from the group consisting of a gene encoding:

(a) a hexose ~~or pentose~~ transporter;

(b) a pentose transporter;

(c) a[[n]] xylulose kinase;

(d) an enzyme from the pentose phosphate pathway,

(e) a glycolytic enzyme, and

(f) an ethanologenic enzyme[[s]].

9. (*currently amended*) A transformed host cell according to claim 7, wherein the genetic modification results in ~~consist of the~~ inactivation of an endogenous ~~genes, whereby the~~ gene which is selected from the group consisting of:

(a) a gene encoding a hexose kinase ~~gene~~;

(b) the *Saccharomyces MIG1* gene; ~~and~~

(c) the *Saccharomyces MIG2* gene;[[s]] and

(d) a gene homologous to (a), (b) or (c) and which hybridizes thereto ~~hybridising homologues thereof~~.

10. (*currently amended*) A transformed host cell according to claim 1 ~~any one of the preceding claims, whereby the host cell~~ that further expresses one or more enzymes that confers on ~~to~~ the ~~host~~ cell the ability to produce lactic acid, acetic acid, succinic acid, amino acids, 1,3-propanediol, ethylene, glycerol, a β-lactam antibiotic[[s]] or ~~and~~ a cephalosporin[[s]].

11. (*currently amended*) A transformed host cell according to claim 10 that further comprises ~~, whereby the host cell contains~~ a genetic modification that results in decreased alcohol dehydrogenase activity.

12. (*currently amended*) A process for producing ethanol, ~~whereby the process comprises~~ comprising the steps of:

(a) fermenting a medium containing a source of xylose with the [[a]] transformed host cell ~~as defined in any one~~ of claim[[s]] 1[[-9]], which ~~whereby the~~ host cell ferments xylose to ethanol, and, optionally,

(b) recovering ~~recovery of~~ the ethanol.

13. (*currently amended*) A process according to claim 12, wherein ~~whereby~~ the medium also contains a source of glucose.

14. (*currently amended*) A process according to claim[[s]] 12 ~~or 13~~, wherein ~~whereby~~ the production ~~volumetric~~ of ethanol ~~productivity is~~ occurs at a rate of at least 0.5 g ethanol per liter ~~litre~~ per hour.

15. (*currently amended*) A process according to ~~claims any one of claims~~ claim 12 [[-14]], wherein ~~whereby~~ the ethanol yield is at least 50 %.

16. (*currently amended*) A process for producing, as a fermentation product, ~~selected from the group consisting of~~ lactic acid, acetic acid, succinic acid, an amino acid[[s]], 1,3-propanediol, ethylene, glycerol, a β-lactam antibiotic[s] or ~~and~~ a cephalosporin[[s]], which ~~whereby the~~ process comprises the steps of:

(a) fermenting a medium containing a source of xylose with the [[a]] transformed host cell ~~as defined in claims~~ of claim 10 ~~or 11~~, ~~whereby the~~ which host cell ferments xylose to yield the fermentation product, and, optionally,

(b) recovering ~~recovery of~~ the fermentation product.

17. (*currently amended*) A process according to claim 16, wherein ~~whereby~~ the medium also contains a source of glucose.

18. *(new)* The yeast cell of claim 2 that is a member of a genus selected from the group consisting of *Saccharomyces*, *Kluyveromyces*, *Candida*, *Pichia, Schizosaccharomyces*, *Hansenula*, *Kloeckera*, *Schwanniomyces*, and *Yarrowia.*

19. *(new)* The filamentous fungus cell of claim 4 that is a member of a genus selected from the group consisting of *Aspergillus*, *Trichoderma*, *Humicola*, *Acremonium*, *Fusarium*, and *Penicillium*.

20. *(new)* The process of claim 16 wherein the host cell further comprises a genetic modification that results in decreased alcohol dehydrogenase activity.